



10-761593-revised-a.ST25
SEQUENCE LISTING



<110> Sun, Lee-Hwei K
Sun, Bill N
Sun, Cecily R

<120> Fc fusion proteins of human erythropoietin with high biological activities

<130> 02SUN2001-A

<140> US 10/761,593

<141> 2004-01-21

<150> 09/932812

<151> 2001-08-17

<160> 28

<170> PatentIn version 3.2

<210> 1

<211> 29

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<223> synthetic

<400> 2

cggatccgtc ccctgtcctg caggcct

27

<210> 3

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<212> DNA

<213> Artificial Sequence

<220>

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<222> (1)..(20)

<223> synthetic

<400> 3

gagcgcaaat gttgtgtcga

20

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 <222> (1)..(28)
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28

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<400> 5
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<400> 6
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<220>
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 <222> (1)..(69)
 <223> synthetic

<400> 7
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 ttgtgtcga

60

69

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<220>
 <221> misc_feature
 <223> Synthetic

<400> 8
 gagtccaaat atggtccccc a 21

<210> 9
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)..(28)
 <223> Synthetic

<400> 9
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<210> 10
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
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 <222> (1)..(21)
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<210> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)..(60)
 <223> Synthetic

<400> 11
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<210> 12
 <211> 70

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<212> DNA
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<220>
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<222> (1)..(70)
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<400> 12
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<221> misc_feature
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<210>	14
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<210>	15
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<223> Synthetic
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<212>	DNA
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 <222> (1)..(70)
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<400> 16
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<210> 17
 <211> 1332
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HuEPO-L-VFc gamma2 (Figure 2A)

<400> 17
 aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc 60
 ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac 120
 agccgagtcc tggagaggta cctcttggag gccaaggagg ccgagaatat cacgacgggc 180
 tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc 240
 tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc 300
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 gagcccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg 420
 cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct 480
 ccactccgaa caatcactgc tgacactttc cgaaaactct tccgagtcta ctccaatttc 540
 ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt 600
 ggcggttccg gtggaggcgg aagcggcggt ggaggatcag agcgcaaata ttgtgtcgag 660
 tgcccaccgt gccagcacc acctgtggca ggaccgtcag tcttcctctt cccccaaaa 720
 cccaaggaca ccctcatgat ctcccggacc cctgagggtca cgtgcgtggg ggtggacgtg 780
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 ggcctcccag cctccatcga gaaaaccatc tccaaaacca aagggcagcc ccgagaacca 1020
 cagggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc 1080
 tgcctgggtca aaggcttcta cccagcgac atcgccgtgg agtgggagag caatgggcag 1140
 ccggagaaca actacaagac cacacctccc atgctggact ccgacggctc cttcttcctc 1200
 tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 1260

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gtgatgcatg aggctctgca caaccactac acgcagaaga gcctctccct gtctccgggt 1320
 aaatgagaat tc 1332

<210> 18
 <211> 436
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2A)

<400> 18

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

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Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
195 200 205

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
210 215 220

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
225 230 235 240

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
245 250 255

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
260 265 270

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
275 280 285

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
290 295 300

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Ser
305 310 315 320

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
325 330 335

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
340 345 350

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
355 360 365

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
370 375 380

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
385 390 395 400

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
405 410 415

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
420 425 430

Ser Pro Gly Lys

435

<210> 19
 <211> 1335
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HuEPO-L-vFc gamma4 (Figure 2B)

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<400> 19
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agccgagtcc tggagaggtg cctcttggag gccaaggagg ccgagaatat cagcaggggc    180
tgtgtgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc    240
tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc    300
ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg    360
gagcccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg    420
cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct    480
ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc    540
ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt    600
ggcggttccg gtggaggcgg aagcggcggg ggaggatcag agtccaaata tggccccca    660
tgcccaccat gcccagcacc tgagttcgcg gggggaccat cagtcttcct gttccccca    720
aaaccaagg acactctcat gatctcccgg acccctgagg tcacgtgcgt ggtggtggac    780
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aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag   1020
ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg   1080
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg   1140
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttcttc   1200
ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc   1260
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctctg   1320
ggtaaatagag aattc                                     1335
  
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<210> 20
 <211> 437
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure 2B)

<400> 20

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 1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Gly ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 195 200 205

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
 210 215 220

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Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
225 230 235 240

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
245 250 255

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
260 265 270

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
305 310 315 320

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
325 330 335

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
340 345 350

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
355 360 365

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
370 375 380

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
385 390 395 400

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
405 410 415

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
420 425 430

Leu Ser Leu Gly Lys
435

<210> 21
<211> 1329
<212> DNA
<213> Artificial Sequence

<220>
<223> HuEPO-L-VFC gamma1 (Figure 2C)

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<400> 21
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agccgagtcc tggagaggta cctcttggag gccaaaggagg ccgagaatat cacgacgggc 180
tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc 240
tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc 300
ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg 360
gagcccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg 420
cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct 480
ccactccgaa caatcactgc tgacactttc cgaaactct tccgagtcta ctccaatttc 540
ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt 600
ggcggttccg gtggaggcgg aagcggcggg ggaggatcag acaaaactca cacatgccc 660
ccgtgcccag cacctgaagt cgcgggggga ccgtcagtct tcctcttccc cccaaaaccc 720
aaggacaccc tcatgatctc ccggacacct gaggtcacat gcgtggtggt ggacgtgagc 780
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggagggt gcataatgcc 840
aagacaaagc cgcgggagga gcagtacaac agcacgtacc ggggtggtcag cgtcctcacc 900
gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggcttc caacaaagcc 960
ctcccagcct ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1020
gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1080
ctgggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 1140
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1200
agcaagctca ccgtggacaa gagcagggtg cagcagggga acgtcttctc atgctccgtg 1260
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 1320
tgagaattc 1329

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<210> 22
<211> 435
<212> PRT
<213> Artificial Sequence

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<220>
<223> HuEPO-L-vFc gamma1 with a 27-amino acid leader peptide (Figure 2C)

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<400> 22
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1          5          10          15

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Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
 20 25 30
 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 35 40 45
 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 50 55 60
 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 65 70 75 80
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 85 90 95
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175
 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190
 Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 195 200 205
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Val Ala Gly
 210 215 220
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 225 230 235 240
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 245 250 255
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 260 265 270

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His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
275 280 285

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
325 330 335

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
340 345 350

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
355 360 365

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
370 375 380

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
385 390 395 400

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
405 410 415

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
420 425 430

Pro Gly Lys
435

<210> 23
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic linker

<400> 23

Gly ser Gly Gly Gly ser Gly Gly Gly Gly ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 24
<211> 15
<212> PRT

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<213> Homo sapiens

<400> 24

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 25

<211> 10

<212> PRT

<213> Homo sapiens

<400> 25

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 26

<211> 232

<212> PRT

<213> Homo sapiens

<400> 26

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
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145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

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<210> 27
<211> 228
<212> PRT
<213> Homo sapiens
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<400> 27

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
100 105 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
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130

135

140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 210 215 220

Ser Pro Gly Lys
 225

<210> 28
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 28

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
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Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225